

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BLOOM, F.
KUO, JONATHAN
LIN, JHY-JHU
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(ii) TITLE OF THE INVENTION: METHOD FOR INCREASING VIABILITY
AND TRANSFORMATION EFFICIENCY OF BACTERIA DURING
STORAGE AT LOW TEMPERATURES

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: DC
(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: U.S. Ser. No. 06/014,330
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(A) APPLICATION NUMBER: U.S. Ser. No. 06/025,838
(B) FILING DATE: 05-SEP-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGACTCACTA TAGCGAACTG ATCCT

25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATTTAGGTG ACACTATAGA GATCC

25

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCACATATCC GGGTTTTTCG CTG

23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAGGTTGGCA GGTGTATGG AGT

23

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TATGGAGCAG GCAATCGCTG ATG

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGTGAAGTGT TCGCGGATAA GAG

23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGCGGCCT CGGCGACTAA CAC

23

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTTACGGTG CGTTGGCAGG ATT

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATCAACGCC ATGCATCGCC ATC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACTCCATACA AACTGCCAAC CTC

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGGCGGCGG CGAAGAG

17

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAATGGCTGA TCGGACTTGT T

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCCGGGGTGT CTTGTATT

19

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGTAGNTTTC	GTTCGATTGG	CGCTCAAACC	CGTATAGCG	CGAGTGACAA	CAACGGGCTG	60
GCAATACCAC	CGCGATAAT	CGCGGCTTTC	CGTTTGTGG	TGCGCGTGG	GTTAAACAC	120
GGCGCGGAGC	AGGGGAGCG	TAATGTCTBT	TGCATCAGC	CGCAAGCAT	TTCCCGTTTG	180
CGCCCAAAGC	CGTTAAGTTT	TTGCATCGTG	AATCGGCTGT	CGTGCAAAAC	CGCGCGGACA	240
AAACCGGCG	ACGTAAATGT	CGCCAGCGTG	CGCGCTGGAC	CGCCCAACCT	TGCCATGGCG	300
TTAAACAGAT	TTTGGCTCCA	CATATCGGG	TTTTTGTGT	CGCCAAAGCC	GTCCAGAAAC	360
CAGGCATCTA	CTTTTGTATT	TAGCGAATCG	TCCAGTTGGC	TGGTCAGTTC	GTTAATATCG	420
CCAAACCAT	AATCCAGCGT	CACGGGGCTT	TGATCGAGCA	ATAAACGATG	GCAACCGGGC	480
AAGGGCATTG	GGTACTGGGC	CTGAAGTTGT	TGTGCTCAG	GAGCGAGTTC	CGGCCAGTGT	540
TGATGCCTTA	AGGCTAAATC	CGCACGGGTG	AGGGGAAATT	TCTCAAAACT	AATGAAATGT	600
AAGCGTTTGA	ATTGCTCTTG	CGGATCGCGT	TGCGGAAACT	BATCAAAATG	CTGCCATAGC	660
GTCCAGGAAT	TTAATCGGCT	GGCGAAGCGG	CTGTCTGTGA	CGCAAAACAG	AGCATGTGGA	720
TGCTCAGGAA	AGCTATAGCT	TAATGTGGTT	CGTCCGAGAA	AAACATAAAG	CGTCTCTTCC	780
AGCGCGTTAT	CGTTGGGAAA	ATAGACATCG	TCAAAATTTG	GGGAAACAGG	TGTACCTTCA	840
GCATTAAATT	CGAGGTTGCT	AGGTTGTATG	GAGTAGTCTT	TCAAGTAAGT	TACTGTCTTT	900
ACAGCGCGTG	CTCTGATCTT	AGCGATGTGT	GTAAGGCTGC	GCMAATTTCT	CTATTAAATG	960
CTTGATCGGA	CTTGTTCGGC	GTACAAGTGT	ACGCTATTTT	GCAATTCGAA	CTTACTCTAT	1020
GTCCGACTTA	CAGAGGTAAT	GAATGAAACG	TGCAGTGAAT	ACTGGGCTGG	GCATTGTTTC	1080
CAGCATCGGT	AATAACTAAG	AGGAAGTCTT	GGCATCTCTG	CGTGAAGGAC	GTTCAGGGAT	1140
CAGTTTCTCT	CAGGAGCTGA	AGGATTCGCG	CATGCGTAGC	CACGTCTCGG	GCAACGTAAA	1200
ACTGGATACC	ACTGGCTCTA	TTGACCGCAA	AGTTGTGGCG	TTTATGAGCG	AGGCATCCAT	1260

TTATGCATTC	CTTTCTATGG	AGCAGGCAAT	CGGTGATGCG	GGCCTCTCTC	CGGAAGCTTA	1320
CCAGAATAAC	CCGCGCGTTG	GCTTGATTGC	AGGTTCCGGG	GGCGGCTCCC	CGCGTTTCCA	1380
GGTGTTCGGC	GCTGACGCAA	TGCGCGGCGC	GCGCGGCGTG	AAAGCGGTTG	GCCCCTATGT	1440
GGTCACCAAA	GCGATGGCAT	CGGGCGTTTC	TGCTTGCTTC	GCGACCCCGT	TTAAAATTCA	1500
TGGCGTTAAC	TACTCCATCA	GCTCCGCGTG	TGCGACTTCC	GCACACTGTA	TCGGTAACGC	1560
AGTAGAGCAG	ATCCAACTGG	GCAAAACAGGA	CATCGTGTTC	CGTGGCGGCG	GCGAAGAGCT	1620
GTGCTGGGAA	ATGGCTTGCG	AATTCGACGC	AATGGGTGCG	CTGTCTACTA	AATACAAACA	1680
CACCCCGGAA	AAAGCCTCCC	GTACTTACCA	CGCTCACCGT	GACGGTTTCG	TTATCGCTGG	1740
CGGCGCGCGT	ATGGTAGTGG	TTGAAGAGCT	GGAACACGCG	CTGGCGCGTG	GTGCTCACAT	1800
CTATGCTGAA	ATCGTTGGCT	ACGGCGCAAC	CTCTGATGCT	GCAGACATGG	TTGCTCCGTC	1860
TGGCGAAGGC	GCAGTACGCT	GCATGAAGAT	GGCGATGCAT	GGCGTTGATA	CCCCAATCGA	1920
TTACCTGAAC	TCCACGGTA	CTTCGACTCC	GGTTGGCGAC	CTGAAAGAGC	TGGCAGCTAT	1980
CCGTGAAGTG	TTGCGCGATA	AGAGCCCGGC	GATTTCTGCA	ACCAAAAGCA	TGACCGGTCA	2040
CTCTCTGGGC	GCTGCTGGCG	TACAGGAAGC	TATCTACTCT	CTGCTGATGC	TGGAACACGG	2100
CTTTATCGCC	CCGAGCATCA	ACATTGAAGA	GCTGGACGAG	CAGGCTGCGG	GTCTGAACAT	2160
CGTGACCGAA	ACGACCGATC	GCGAACTGAT	CACCGTTATG	TCTAACAGCT	TCGGCTTCGG	2220
CGGCACCAAC	GCGACGCTGG	TAATGCGCAA	GCTGAAAGAT	TAATTCGAG	TAGGTGCGAG	2280
TAGACCGCGC	AGCCTCGCAT	CGGACGTTAC	GCGGCAATGC	CGCCTCCGGC	ACTAACGCAA	2340
AAGGGAACCT	GATGGTTCCC	TTTTTCACAT	CATTGACAA	CGCGCGCAGT	TCCAGGCAAA	2400
CTTCCCGCTT	TGTCGATTTC	CTTCTGAAAA	GACGTACGCG	TTAAATCGTG	CCAAACGCACC	2460
GTAACCTCTGA	AACGAGAGAG	ATGAGACGGG	GATACTCTTC	GCCTTGCGCT	GCATTCTGGA	2520
GTAATGCATG	ACTGCTGTAA	GCGAAACCGA	AACACGATCT	TTCTGCCAAT	TTTTGCTGTT	2580
TTCCGCACTG	CTTTTTCGCG	TTTTTCTTCA	CTACATGAC	CGGTAGGCTT	GCCGTTGCGG	2640
GTATCCCGCG	TGTTTGTG					2658

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAAATTCGAG GTTGCGAGGT T

21

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATCGACAAA GCGCGAAGTT

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTCTCTGGGC	GCTGCTGGCG	TACAGGAAGC	TATCTACTCT	CTGCTGATGC	TGGAACACGG	60
CTTTATCGCC	CCGAGCATCA	ACATTGAAGA	GCTGGACGAG	CAGGCTGCGG	GTCTGAACAT	120
CGTGACCGA						129